ABSTRACT

The invention disclosed in this application provides methods of diagnosing and treating stress urinary incontinence and predisposition to stress urinary incontinence. These methods are based on the identification of significant differences in gene expression in the pelvic supporting tissues of premenopausal women afflicted with SUI as compared with continent, control women, using microarray-based techniques. The identified differences in gene expression may contribute to altered ECM metabolism and ECM remodeling in pelvic tissue from SUI women. The invention also provides candidate genes for use in diagnosing disorders characterized by pelvic floor dysfunction, including SUI, identification of therapeutic gene targets, evaluation of treatment regimens, prediction of treatment outcome, design of therapeutic agents, and identification of individuals at risk for developing these disorders. Various embodiments of the present invention are disclosed which relate to the above-described uses of candidate genes.